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Watershed-driven relaxation labeling for image segmenta

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Abstract

Introduces an image **segmentation** method referred to as **watershed-driven relaxation la** is a hybrid **segmentation** process utilizing both **watershed** analysis and relaxation labelin **watershed** analysis is used to subdivide an image into catchment basins, effectively clust based on their spatial proximity and intensity homogeneity. Classification estimates in the are set for each of these catchment basins. Relaxation labeling is then used to iteratively r classifications of the catchment basins through propagating constraints and utilizing local i relaxation updating process is continued until a large majority of the catchment basins are classified. The method provides fast, accurate **segmentation** results and exploits the indiv **watershed** analysis and relaxation labeling. The robustness of the method is illustrated th to other popular **segmentation** techniques

Index Terms

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[catchment basins](#) [classifications](#) [hybrid segmentation process](#) [image classifica](#)
[segmentation](#) [intensity homogeneity](#) [iterative methods](#) [local information](#) [prop](#)
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[watershed analysis](#) [watershed-driven relaxation labeling](#)

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Cooperation of color pixel classification schemes and color watershed segmentation: a study for microscopic images

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Abstract

We study the ability of the cooperation of two-color pixel classification schemes (Bayesian classification) with color watershed. Using color pixel classification alone does not suffice to extract color regions so we suggest to use a strategy based on three steps: simplification, color watershed. Color watershed is based on a new aggregation function using local and global criteria. The strategy is performed on microscopic images. Quantitative measures are used to evaluate segmentations according to a learning set of reference images.

Index Terms

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[Bayesian classification](#) [K-means classification](#) [aggregation function](#) [color pixel classification](#) [color regions extraction](#) [color watershed](#) [global criteria](#) [image segmentation](#) [learning set](#) [local criteria](#) [microscopic images](#) [reference image](#)
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Model-based morphological segmentation and labeling of angiograms

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Abstract

A method for extraction and labeling of the coronary arterial tree (CAT) using minimal user single-view angiograms is proposed. The CAT structural description (skeleton and borders with quantitative information for the artery dimensions and assignment of coded labels, based on a coronary artery model represented by a graph. The stages of the method are: (1) CAT tracking; (2) artery skeleton and border estimation; (3) feature graph creation; and (iv) artery labeling. The approximate CAT centerline and borders are extracted by recursive tracking based on analysis. The accurate skeleton and borders of each CAT segment are computed, based on homotopy modification and watershed transform. The approximate centerline and borders are used for constructing the artery segment enclosing area (ASEA), where the defined skeleton and borders are considered as markers. Using the marked ASEA, an artery gradient image is constructed. The pixels (except the skeleton ones) are assigned the gradient magnitude of the original image. The gradient image markers are imposed as its unique regional minima by the homotopy modification. Finally, the watershed transform is used for extracting the artery segment borders, and the feature graph is created. Finally, given the created feature graph and the known model graph, a graph matching algorithm is used to assign appropriate labels to the extracted CAT using weighted maximal cliques on the association graph. Experimental results using clinical digitized coronary angiograms are presented.

Index Terms

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[angiocardiology](#) [diagnostic radiography](#) [edge detection](#) [feature extraction](#) [theory](#) [image segmentation](#) [medical image processing](#) [physiological models](#)

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An improved watershed algorithm for counting objects in anisotropic 3-D biological images

Ancin, H. Dufresne, T.E. Ridder, G.M. Turner, J.N. Roysam, B.
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Abstract

Effective 3-D image processing algorithms are presented for automatic counting and analysis of anisotropic 3-D biological images that are collected by laser-scanning confocal microscopy instruments, the x-y resolution is much better than the resolution along the z axis, hence the images (3-D) are anisotropic. In this work, the images are pre-processed by a 3-D extension of an algorithm, and the resulting images are binarized by a clustering based segmentation algorithm. For binary segmentation, some regions consist of individual objects while others are multi-object clusters. The extension of Vincent and Soille's watershed algorithm (1991) to anisotropic 3D spaces is used to segment such cell clusters. The watershed algorithm is applied on marker functions that are generated by a combination of 3-D morphological inverse distance functions and 3-D image gradients. Cell parameters such as volume, average intensity and locations, are calculated on the result of watershed segmentation. The watershed algorithm has been successfully applied to the automated analysis of cell populations from biological studies involving large numbers of tissue samples.

Index Terms

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